RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _09/655,109A_

Source: _1FW/6_

Date Processed by STIC: _7/22/05_

ENTERED

IFW16

RAW SEQUENCE LISTING   DATE: 07/22/2005
PATENT APPLICATION: US/09/655,109A   TIME: 14:47:29

Input Set : **A:\sequence listing.ST25.txt**
Output Set: **N:\CRF4\07222005\I655109A.raw**

```
 3 <110> APPLICANT: H. M. Noteborn , Mathieu
 4        AAM Danen Van Oorschot, Astrid
 6 <120> TITLE OF INVENTION: APOPTIN ASSOCIATING PROTEINS
 8 <130> FILE REFERENCE: 2906-4996US
10 <140> CURRENT APPLICATION NUMBER: 09/655,109A
11 <141> CURRENT FILING DATE: 2000-09-05
13 <150> PRIOR APPLICATION NUMBER: 99203465.2
14 <151> PRIOR FILING DATE: 1999-10-21
16 <160> NUMBER OF SEQ ID NOS: 7
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 17
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial
25 <220> FEATURE:
26 <223> OTHER INFORMATION: pACT-specific 17-mer
28 <400> SEQUENCE: 1
29 taccactaca atggatg                                          17
32 <210> SEQ ID NO: 2
33 <211> LENGTH: 10
34 <212> TYPE: PRT
35 <213> ORGANISM: Artificial
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Myc-tag
41 <220> FEATURE:
42 <221> NAME/KEY: SITE
43 <222> LOCATION: (1)..(10)
45 <400> SEQUENCE: 2
47 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
48 1               5                   10
51 <210> SEQ ID NO: 3
52 <211> LENGTH: 16
53 <212> TYPE: PRT
54 <213> ORGANISM: Artificial
56 <220> FEATURE:
57 <223> OTHER INFORMATION: AAP-1 Peptide
60 <220> FEATURE:
61 <221> NAME/KEY: SITE
62 <222> LOCATION: (1)..(16)
64 <400> SEQUENCE: 3
66 Cys Thr Lys Thr Ser Glu Thr Asn His Thr Ser Arg Pro Arg Leu Lys
67 1               5                   10                  15
70 <210> SEQ ID NO: 4
```

RAW SEQUENCE LISTING   DATE: 07/22/2005
PATENT APPLICATION: US/09/655,109A   · TIME: 14:47:29

Input Set : A:\sequence listing.ST25.txt
Output Set: N:\CRF4\07222005\I655109A.raw

```
 71 <211> LENGTH: 947
 72 <212> TYPE: DNA
 73 <213> ORGANISM: homo sapiens
 75 <220> FEATURE:
 76 <223> OTHER INFORMATION: AAP-1-a nucleic acid
 78 <220> FEATURE:
 79 <221> NAME/KEY: misc_feature
 80 <222> LOCATION: (5)..(5)
 81 <223> OTHER INFORMATION: n can be a, c, g or t
 83 <220> FEATURE:
 84 <221> NAME/KEY: misc_feature
 85 <222> LOCATION: (145)..(145)
 86 <223> OTHER INFORMATION: n can be a, c, g or t
 88 <400> SEQUENCE: 4
```

W--> 89 accanaccca aaaaaagaga tctggaattc ggatcctcga ggccacgaag gccgaaacag   60
```
 91 tgctgaagcc tttaaatgca gcatctgcga tgtgaggaaa ggcacctcca ccagaaaacc     120
 93 tcggatcaat tctcagctgg tggcncaaca agtggcacaa cagtatgcca ccccaccacc     180
 95 ccctaaaaag gagaagaagg agaaagttga aaagcaggac aaagagaaac ctgagaaaga     240
 97 caaggaaatt agtcctagtg ttaccaagaa aaataccaac aagaaaacca aaccaaagtc     300
 99 tgacattctg aaagatcctc ctagtgaagc aaacagcata cagtctgcaa atgctacaac     360
101 aaagaccagc gaaacaaatc acacctcaag gccccggctg aaaaacgtgg acaggagcac     420
103 tgcacagcag ttggcagtaa ctgtgggcaa cgtcaccgtc attatcacag actttaagga     480
105 aaagactcgc tcctcatcga catcctcatc cacagtgacc tccagtgcag ggtcagaaca     540
107 gcagaaccag ascagctcgg ggtcagagag cacagacaag ggctcctccc gttcctccac     600
109 gccaaagggc gacatgtcag cagtcaatga tgaatctttc tgaaattgca catggaattg     660
111 tgaaaactat gaatcagggt atgaaattca aaacctccac ctgcccatgc tgcttgcatc     720
113 cctggagaat cttctgtgga catcgacctc ttagtgatgc tgccaggata atttctgctt     780
115 gccatgggca tctggccacc aaggaatttc gcaccctgac gattactctt gacactttta     840
117 tgtattccat tgttttatat gattttccta acaatcattt ataattggat gtgctcctga     900
119 atctactttt tataaaaaaa gccttygtgg cctcgagaga tctatga                  947
122 <210> SEQ ID NO: 5
123 <211> LENGTH: 1131
124 <212> TYPE: DNA
125 <213> ORGANISM: Homo sapiens
127 <220> FEATURE:
128 <223> OTHER INFORMATION: AAP-1-b nucleic acid
130 <400> SEQUENCE: 5
131 tataactatc tattcgatga tgaagatacc ccaccaaacc caaaaaaaga gatctggaat      60
133 tcggatcctc gaggccacga aggcctttct cctccgagcg gcgccggttt cggcttgggg     120
135 ggggcggggt acagcccatc catgaccatg ggcgacaaga agagcccgac caggccaaaa     180
137 agacaagcga aacctgccgc agacgaaggg ttttgggatt gtagcgtctg caccttcaga     240
139 aacagtgctg aagcctttaa atgcagcatc tgcgatgtga ggaaaggcac ctccaccaga     300
141 aaacctcgga tcaattctca gctggtggca caacaagtgg cacaacagta tgccacccca     360
143 ccaccccta aaaaggagaa gaaggagaaa gttgaaaagc aggacaaaga gaaacctgag     420
145 aaagacaagg aaattagtcc tagtgttacc aagaaaaata ccaacaagaa aaccaaacca     480
147 aagtctgaca ttctgaaaga tcctcctagt gaagcaaaca gcatacagtc tgcaaatgct     540
149 acaacaaaga ccagcgaaac aaatcacacc tcaaggcccc ggctgaaaaa cgtggacagg     600
151 agcactgcac agcagttggc agtaactgtg gcaacgtca ccgtcattat cacagacttt     660
153 aaggaaaaga ctcgctcctc atcgacatcc tcatccacag tgacctccag tgcagggtca     720
```

```
155 gaacagcaga accagagcag ctcggggtca gagagcacag acaagggctc ctcccgttcc    780
157 tccacgccaa agggcgacat gtcagcagtc aatgatgaat ctttgtgaaa ttgcacatgg    840
159 aattgtgaaa actatgaatc agggtatgaa attcaaaacc tccacctgcc catgctgctt    900
161 gcatccctgg agaatcttct gtggacatcg acctcttagt gatgctgcca ggataatttc    960
163 tgcttgccat gggcatctgg ccaccaagga atttcgcacc ctgacgatta ctcttgacac   1020
165 ttttatgtat tccattgttt tatatgattt tcctaacaat catttataat tggatgtgct   1080
167 cctgaatcta cttttttataa aaaggccttc gtggcctcga gagatctatg a           1131
170 <210> SEQ ID NO: 6
171 <211> LENGTH: 352
172 <212> TYPE: PRT
173 <213> ORGANISM: Homo sapiens
176 <220> FEATURE:
177 <221> NAME/KEY: MISC_FEATURE
178 <222> LOCATION: (251)..(251)
179 <223> OTHER INFORMATION: X is an unknown amino acid
181 <220> FEATURE:
182 <221> NAME/KEY: MISC_FEATURE
183 <222> LOCATION: (288)..(289)
184 <223> OTHER INFORMATION: X is an unknown amino acid
186 <220> FEATURE:
187 <221> NAME/KEY: MISC_FEATURE
188 <222> LOCATION: (314)..(314)
189 <223> OTHER INFORMATION: X is an unknown amino acid
191 <220> FEATURE:
192 <221> NAME/KEY: MISC_FEATURE
193 <222> LOCATION: (324)..(324)
194 <223> OTHER INFORMATION: X is an unknown amino acid
196 <220> FEATURE:
197 <221> NAME/KEY: MISC_FEATURE
198 <222> LOCATION: (327)..(327)
199 <223> OTHER INFORMATION: X is an unknown amino acid
201 <220> FEATURE:
202 <221> NAME/KEY: MISC_FEATURE
203 <222> LOCATION: (352)..(352)
204 <223> OTHER INFORMATION: X is an unknown amino acid
206 <400> SEQUENCE: 6
208 His Glu Gly Leu Ser Pro Pro Ser Gly Ala Gly Phe Gly Leu Gly Gly
209 1               5                   10                  15
212 Ala Gly Tyr Ser Pro Ser Met Thr Met Gly Asp Lys Lys Ser Pro Thr
213             20                  25                  30
216 Arg Pro Lys Arg Gln Ala Lys Pro Ala Ala Asp Glu Gly Phe Trp Asp
217         35                  40                  45
220 Cys Ser Val Cys Thr Phe Arg Asn Ser Ala Glu Ala Phe Lys Cys Ser
221     50                  55                  60
224 Ile Cys Asp Val Arg Lys Gly Thr Ser Thr Arg Lys Pro Arg Ile Asn
225 65                  70                  75                  80
228 Ser Gln Leu Val Ala Gln Gln Val Ala Gln Gln Tyr Ala Thr Pro Pro
229                 85                  90                  95
232 Pro Pro Lys Lys Glu Lys Lys Glu Lys Val Glu Lys Gln Asp Lys Glu
```

```
                RAW SEQUENCE LISTING              DATE: 07/22/2005
                PATENT APPLICATION:  US/09/655,109A      TIME: 14:47:29

                Input Set : A:\sequence listing.ST25.txt
                Output Set: N:\CRF4\07222005\I655109A.raw

233                   100                    105                    110
236 Lys Pro Glu Lys Asp Lys Glu Ile Ser Pro Ser Val Thr Lys Lys Asn
237           115                   120                    125
240 Thr Asn Lys Lys Thr Lys Pro Lys Ser Asp Ile Leu Lys Asp Pro Pro
241       130                   135                    140
244 Ser Glu Ala Asn Ser Ile Gln Ser Ala Asn Ala Thr Thr Lys Thr Ser
245 145                   150                    155                    160
248 Glu Thr Asn His Thr Ser Arg Pro Arg Leu Lys Asn Val Asp Arg Ser
249                   165                   170                    175
252 Thr Ala Gln Gln Leu Ala Val Thr Val Gly Asn Val Thr Val Ile Ile
253           180                   185                    190
256 Thr Asp Phe Lys Glu Lys Thr Arg Ser Ser Ser Thr Ser Ser Ser Thr
257           195                   200                    205
260 Val Thr Ser Ser Ala Gly Ser Glu Gln Gln Asn Gln Ser Ser Ser Gly
261       210                   215                    220
264 Ser Glu Ser Thr Asp Lys Gly Ser Ser Arg Ser Ser Thr Pro Lys Gly
265 225                   230                    235                    240
W--> 268 Asp Met Ser Ala Val Asn Asp Glu Ser Phe Xaa Asn Cys Thr Trp Asn
269                   245                   250                    255
272 Cys Glu Asn Tyr Glu Ser Gly Tyr Glu Ile Gln Asn Leu His Leu Pro
273           260                   265                    270
276 Met Leu Leu Ala Ser Leu Glu Asn Leu Leu Trp Thr Ser Thr Ser Xaa
277           275                   280                    285
280 Xaa Cys Cys Gln Asp Asn Phe Cys Leu Pro Trp Ala Ser Gly His Gln
281       290                   295                    300
284 Gly Ile Ser His Pro Asp Asp Tyr Ser Xaa His Phe Tyr Val Phe His
285 305                   310                    315                    320
288 Cys Phe Ile Xaa Phe Ser Xaa Gln Ser Phe Ile Ile Gly Cys Ala Pro
289                   325                   330                    335
292 Glu Ser Thr Phe Tyr Lys Lys Ala Phe Val Ala Ser Arg Asp Leu Xaa
293           340                   345                    350
296 <210> SEQ ID NO: 7
297 <211> LENGTH: 8
298 <212> TYPE: PRT
299 <213> ORGANISM: Simian virus 40
301 <220> FEATURE:
302 <223> OTHER INFORMATION: SV40 large T antigen
304 <400> SEQUENCE: 7
306 Pro Pro Lys Lys Lys Arg Lys Val
307 1               5
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/22/2005
PATENT APPLICATION: US/09/655,109A   TIME: 14:47:30

Input Set : **A:\sequence listing.ST25.txt**
Output Set: **N:\CRF4\07222005\I655109A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 5,145
Seq#:6; Xaa Pos. 251,288,289,314,324,327,352

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3

VERIFICATION SUMMARY   DATE: 07/22/2005
PATENT APPLICATION: **US/09/655,109A**   TIME: 14:47:30

Input Set : **A:\sequence listing.ST25.txt**
Output Set: **N:\CRF4\07222005\I655109A.raw**

L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
M:341 Repeated in SeqNo=4
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:240
M:341 Repeated in SeqNo=6